

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Troutt, Anthony

(ii) TITLE OF INVENTION:

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(iii) NUMBER OF SEQUENCES: 4

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation

(B) STREET: 51 University Street

(C) CITY: Seattle

(D) STATE: WA

(E) COUNTRY: USA

(F) ZIP: 98101

20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: Apple PowerMacintosh

(C) OPERATING SYSTEM: Apple Operating System 7.5.5

(D) SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: -to be assigned-

(B) FILING DATE:

(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: USSN 60/052,525

(B) FILING DATE: 27 NOVEMBER 1996

(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perkins, Patricia Anne

(B) REGISTRATION NUMBER: 34,693

(C) REFERENCE/DOCKET NUMBER: 2623-A

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430

(B) TELEFAX: (206)

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA to mRNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse
(B) CLONE: IL-17 receptor

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 121..2712

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA ACGAGACGAC CTGCTGCCGA CGAGCGCCAG TCCTCGGCCG GGAAAGCCAT 60
 CGCGGGCCCT CGCTGTCGCG CGGAGCCAGC TGCGAGCGCT CCGCGACCGG GCCGAGGGCT 120
 15 ATG GCG ATT CGG CGC TGC TGG CCA CGG GTC GTC CCC GGG CCC GCG CTG 168
 Met Ala Ile Arg Arg Cys Trp Pro Arg Val Val Pro Gly Pro Ala Leu
 1 5 10 15
 20 GGA TGG CTG CTT CTG CTG CTG AAC GTT CTG GCC CCG GGC CGC GCC TCC 216
 Gly Trp Leu Leu Leu Leu Leu Asn Val Leu Ala Pro Gly Arg Ala Ser
 20 25 30
 25 CCG CGC CTC CTC GAC TTC CCG GCT CCG GTC TGC GCG CAG GAG GGG CTG 264
 Pro Arg Leu Leu Asp Phe Pro Ala Pro Val Cys Ala Gln Glu Gly Leu
 35 40 45
 30 AGC TGC AGA GTC AAG AAT AGT ACT TGT CTG GAT GAC AGC TGG ATC CAC 312
 Ser Cys Arg Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
 50 55 60
 35 CCC AAA AAC CTG ACC CCG TCT TCC CCA AAA AAC ATC TAT ATC AAT CTT 360
 Pro Lys Asn Leu Thr Pro Ser Ser Pro Lys Asn Ile Tyr Ile Asn Leu
 65 70 75 80
 40 AGT GTT TCC TCT ACC CAG CAC GGA GAA TTA GTC CCT GTG TTG CAT GTT 408
 Ser Val Ser Ser Thr Gln His Gly Glu Leu Val Pro Val Leu His Val
 85 90 95
 45 GAG TGG ACC CTG CAG ACA GAT GCC AGC ATC CTG TAC CTC GAG GGT GCA 456
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
 100 105 110
 50 GAG CTG TCC GTC CTG CAG CTG AAC ACC AAT GAG CGG CTG TGT GTC AAG 504
 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Lys
 115 120 125
 55 TTC CAG TTT CTG TCC ATG CTG CAG CAT CAC CGT AAG CGG TGG CGG TTT 552
 Phe Gln Phe Leu Ser Met Leu Gln His His Arg Lys Arg Trp Arg Phe
 130 135 140
 TCC TTC AGC CAC TTT GTG GTA GAT CCT GGC CAG GAG TAT GAA GTG ACT 600
 Ser Phe Ser His Phe Val Val Asp Pro Gly Gln Glu Tyr Glu Val Thr
 145 150 155 160
 648 GTT CAC CAC CTG CCG AAG CCC ATC CCT GAT GGG GAC CCA AAC CAC AAA
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Lys
 165 170 175

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	TCC AAG ATC ATC TTT GTG CCT GAC TGT GAG GAC AGC AAG ATG AAG ATG	696
	Ser Lys Ile Ile Phe Val Pro Asp Cys Glu Asp Ser Lys Met Lys Met	
	180 185 190	
5	ACT ACC TCA TGC GTG AGC TCA GGC AGC CTT TGG GAT CCC AAC ATC ACT	744
	Thr Thr Ser Cys Val Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr	
	195 200 205	
10	GTG GAG ACC TTG GAC ACA CAG CAT CTG CGA GTG GAC TTC ACC CTG TGG	792
	Val Glu Thr Leu Asp Thr Gln His Leu Arg Val Asp Phe Thr Leu Trp	
	210 215 220	
15	AAT GAA TCC ACC CCC TAC CAG GTC CTG CTG GAA AGT TTC TCC GAC TCA	840
	Asn Glu Ser Thr Pro Tyr Gln Val Leu Leu Glu Ser Phe Ser Asp Ser	
	225 230 235 240	
20	GAG AAC CAC AGC TGC TTT GAT GTC GTT AAA CAA ATA TTT GCG CCC AGG	888
	Glu Asn His Ser Cys Phe Asp Val Val Lys Gln Ile Phe Ala Pro Arg	
	245 250 255	
25	CAA GAA GAA TTC CAT CAG CGA GCT AAT GTC ACA TTC ACT CTA AGC AAG	936
	Gln Glu Glu Phe His Gln Arg Ala Asn Val Thr Phe Thr Leu Ser Lys	
	260 265 270	
30	TTT CAC TGG TGC TGC CAT CAC CAC GTG CAG GTC CAG CCC TTC TTC AGC	984
	Phe His Trp Cys Cys His His His Val Gln Val Gln Pro Phe Phe Ser	
	275 280 285	
35	AGC TGC CTA AAT GAC TGT TTG AGA CAC GCT GTG ACT GTG CCC TGC CCA	1032
	Ser Cys Leu Asn Asp Cys Leu Arg His Ala Val Thr Val Pro Cys Pro	
	290 295 300	
40	GTA ATC TCA AAT ACC ACA GTT CCC AAG CCA GTT GCA GAC TAC ATT CCC	1080
	Val Ile Ser Asn Thr Thr Val Pro Lys Pro Val Ala Asp Tyr Ile Pro	
	305 310 315 320	
45	CTG TGG GTG TAT GGC CTC ATC ACA CTC ATC GCC ATT CTG CTG GTG GGA	1128
	Leu Trp Val Tyr Gly Leu Ile Thr Leu Ile Ala Ile Leu Leu Val Gly	
	325 330 335	
50	TCT GTC ATC GTG CTG ATC ATC TGT ATG ACC TGG AGG CTT TCT GGC GCC	1176
	Ser Val Ile Val Leu Ile Ile Cys Met Thr Trp Arg Leu Ser Gly Ala	
	340 345 350	
55	GAT CAA GAG AAA CAT GGT GAT GAC TCC AAA ATC AAT GGC ATC TTG CCC	1224
	Asp Gln Glu Lys His Gly Asp Asp Ser Lys Ile Asn Gly Ile Leu Pro	
	355 360 365	
60	GTA GCA GAC CTG ACT CCC CCA CCC CTG AGG CCC AGG AAG GTC TGG ATC	1272
	Val Ala Asp Leu Thr Pro Pro Pro Leu Arg Pro Arg Lys Val Trp Ile	
	370 375 380	
65	GTC TAC TCG GCC GAC CAC CCC CTC TAT GTG GAG GTG GTC CTA AAG TTC	1320
	Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu Val Val Leu Lys Phe	
	385 390 395 400	
70	GCC CAG TTC CTG ATC ACT GCC TGT GGC ACT GAA GTA GCC CTT GAC CTC	1368
	Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu Val Ala Leu Asp Leu	
	405 410 415	

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	CTG GAA GAG CAG GTT ATC TCT GAG GTG GGG GTC ATG ACC TGG GTG AGC	1416
	Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val Met Thr Trp Val Ser	
	420 425 430	
5	CGA CAG AAG CAG GAG ATG GTG GAG AGC AAC TCC AAA ATC ATC ATC CTG	1464
	Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Ile Leu	
	435 440 445	
10	TGT TCC CGA GGC ACC CAA GCA AAG TGG AAA GCT ATC TTG GGT TGG GCT	1512
	Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala Ile Leu Gly Trp Ala	
	450 455 460	
15	GAG CCT GCT GTC CAG CTA CGG TGT GAC CAC TGG AAG CCT GCT GGG GAC	1560
	Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp Lys Pro Ala Gly Asp	
	465 470 475 480	
	CTT TTC ACT GCA GCC ATG AAC ATG ATC CTG CCA GAC TTC AAG AGG CCA	1608
	Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro	
	485 490 495	
20	GCC TGC TTC GGC ACC TAC GTT GTT TGC TAC TTC AGT GGC ATC TGT AGT	1656
	Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser Gly Ile Cys Ser	
	500 505 510	
25	GAG AGG GAT GTC CCC GAC CTC TTC AAC ATC ACC TCC AGG TAC CCA CTC	1704
	Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr Ser Arg Tyr Pro Leu	
	515 520 525	
30	ATG GAC AGA TTT GAG GAG GTT TAC TTC CGG ATC CAG GAC CTG GAG ATG	1752
	Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met	
	530 535 540	
35	TTT GAA CCC GGC CGG ATG CAC CAT GTC AGA GAG CTC ACA GGG GAC AAT	1800
	Phe Glu Pro Gly Arg Met His His Val Arg Glu Leu Thr Gly Asp Asn	
	545 550 555 560	
	TAC CTG CAG AGC CCT AGT GGC CGG CAG CTC AAG GAG GCT GTG CTT AGG	1848
	Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys Glu Ala Val Leu Arg	
	565 570 575	
40	TTC CAG GAG TGG CAA ACC CAG TGC CCC GAC TGG TTC GAG CGT GAG AAC	1896
	Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp Phe Glu Arg Glu Asn	
	580 585 590	
45	CTC TGC TTA GCT GAT GGC CAA GAT CTT CCC TCC CTG GAT GAA GAA GTG	1944
	Leu Cys Leu Ala Asp Gly Gln Asp Leu Pro Ser Leu Asp Glu Glu Val	
	595 600 605	
50	TTT GAA GAC CCA CTG CTG CCA CCA GGG GGA GGA ATT GTC AAA CAG CAG	1992
	Phe Glu Asp Pro Leu Leu Pro Pro Gly Gly Gly Ile Val Lys Gln Gln	
	610 615 620	
55	CCC CTG GTG CGG GAA CTC CCA TCT GAC GGC TGC CTT GTG GTA GAT GTC	2040
	Pro Leu Val Arg Glu Leu Pro Ser Asp Gly Cys Leu Val Val Asp Val	
	625 630 635 640	
60	TGT GTC AGT GAG GAA GAA AGT AGA ATG GCA AAG CTG GAC CCT CAG CTA	2088
	Cys Val Ser Glu Glu Glu Ser Arg Met Ala Lys Leu Asp Pro Gln Leu	
	645 650 655	

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	TGG CCA CAG AGA GAG CTA GTG GCT CAC ACC CTC CAA AGC ATG GTG CTG	2136
	Trp Pro Gln Arg Glu Leu Val Ala His Thr Leu Gln Ser Met Val Leu	
	660 665 670	
5	CCA GCA GAG CAG GTC CCT GCA GCT CAT GTG GTG GAG CCT CTC CAT CTC	2184
	Pro Ala Glu Gln Val Pro Ala Ala His Val Val Glu Pro Leu His Leu	
	675 680 685	
10	CCA GAC GGC AGT GGA GCA GCT GCC CAG CTG CCC ATG ACA GAG GAC AGC	2232
	Pro Asp Gly Ser Gly Ala Ala Ala Gln Leu Pro Met Thr Glu Asp Ser	
	690 695 700	
15	GAG GCT TGC CCG CTG CTG GGG GTC CAG AGG AAC AGC ATC CTT TGC CTC	2280
	Glu Ala Cys Pro Leu Leu Gly Val Gln Arg Asn Ser Ile Leu Cys Leu	
	705 710 715 720	
	CCC GTG GAC TCA GAT GAC TTG CCA CTC TGT AGC ACC CCA ATG ATG TCA	2328
	Pro Val Asp Ser Asp Asp Leu Pro Leu Cys Ser Thr Pro Met Met Ser	
	725 730 735	
20	CCT GAC CAC CTC CAA GGC GAT GCA AGA GAG CAG CTA GAA AGC CTA ATG	2376
	Pro Asp His Leu Gln Gly Asp Ala Arg Glu Gln Leu Glu Ser Leu Met	
	740 745 750	
25	CTC TCG GTG CTG CAG CAG AGC CTG AGT GGA CAG CCC CTG GAG AGC TGG	2424
	Leu Ser Val Leu Gln Gln Ser Leu Ser Gly Gln Pro Leu Glu Ser Trp	
	755 760 765	
30	CCG AGG CCA GAG GTG GTC CTC GAG GGC TGC ACA CCC TCT GAG GAG GAG	2472
	Pro Arg Pro Glu Val Val Leu Glu Gly Cys Thr Pro Ser Glu Glu Glu	
	770 775 780	
	CAG CGG CAG TCG GTG CAG TCG GAC CAG GGC TAC ATC TCC AGG AGC TCC	2520
	Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser Ser	
	785 790 795 800	
35	CCG CAG CCC CCC GAG TGG CTC ACG GAG GAG GAA GAG CTA GAA CTG GGT	2568
	Pro Gln Pro Pro Glu Trp Leu Thr Glu Glu Glu Glu Leu Glu Leu Gly	
	805 810 815	
40	GAG CCC GTT GAG TCT CTC TCT CCT GAG GAA CTA CGG AGC CTG AGG AAG	2616
	Glu Pro Val Glu Ser Leu Ser Pro Glu Glu Leu Arg Ser Leu Arg Lys	
	820 825 830	
45	CTC CAG AGG CAG CTT TTC TTC TGG GAG CTC GAG AAG AAC CCT GGC TGG	2664
	Leu Gln Arg Gln Leu Phe Phe Trp Glu Leu Glu Lys Asn Pro Gly Trp	
	835 840 845	
50	AAC AGC TTG GAG CCA CGG AGA CCC ACC CCA GAA GAG CAG AAT CCC TCC	2712
	Asn Ser Leu Glu Pro Arg Arg Pro Thr Pro Glu Glu Gln Asn Pro Ser	
	850 855 860	
	TAG GCCTCCTGAG CCTGCTACTT AAGAGGGTGT ATATTGTACT CTGTGTGTGC	2765
55	GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT	2825
	GTGTGTGTGT TAGCCCGGCTT AGAAATGTGA ACATCTGAAT CTGACATAGT GTTGTATAACC	2885
	TGAAGTCCCA GCACTTGGA ACTGAGACTT GATGATCTCC TGAAGCCAGG TGTTTCAGGGC	2945
60	CAGTGTGAAA ACATAGCAAG ACCTCAGAGA AATCAATGCA GACATCTTGG TACTGATCCC	3005

TAAACACACC CCTTTCCCTG ATAACCCGAC ATGAGCATCT GGTCATCATT GCACAAGAAT 3065
 CCACAGCCCCG TTCCCAGAGC TCATAGCCAA GTGTGTTGCT CATTCTTGA ATATTTATTC 3125
 5 TGTACCTACT ATTCATCAGA CATTTGGAAT TCAAAAACAA GTTACATGAC ACAGCCTTAG 3185
 CCACTAAGAA GCTTAAAATT CGGTAAGGAT GTAAAATTAG CCAGGATGAA TAGAGGGCTG 3245
 10 CTGCCCTGGC TGCAGAAGAG CAGGTCGTCT CGTTCCAGTC GAC 3288

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 864 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Ala Ile Arg Arg Cys Trp Pro Arg Val Val Pro Gly Pro Ala Leu
 1 5 10 15
 Gly Trp Leu Leu Leu Leu Leu Asn Val Leu Ala Pro Gly Arg Ala Ser
 20 25 30
 30 Pro Arg Leu Leu Asp Phe Pro Ala Pro Val Cys Ala Gln Glu Gly Leu
 35 40 45
 Ser Cys Arg Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
 50 55 60
 35 Pro Lys Asn Leu Thr Pro Ser Ser Pro Lys Asn Ile Tyr Ile Asn Leu
 65 70 75 80
 40 Ser Val Ser Ser Thr Gln His Gly Glu Leu Val Pro Val Leu His Val
 85 90 95
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
 100 105 110
 45 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Lys
 115 120 125
 Phe Gln Phe Leu Ser Met Leu Gln His His Arg Lys Arg Trp Arg Phe
 130 135 140
 50 Ser Phe Ser His Phe Val Val Asp Pro Gly Gln Glu Tyr Glu Val Thr
 145 150 155 160
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Lys
 165 170 175
 55 Ser Lys Ile Ile Phe Val Pro Asp Cys Glu Asp Ser Lys Met Lys Met
 180 185 190
 60 Thr Thr Ser Cys Val Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
 195 200 205

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Val Glu Thr Leu Asp Thr Gln His Leu Arg Val Asp Phe Thr Leu Trp
 210 215 220
 5 Asn Glu Ser Thr Pro Tyr Gln Val Leu Leu Glu Ser Phe Ser Asp Ser
 225 230 235 240
 Glu Asn His Ser Cys Phe Asp Val Val Lys Gln Ile Phe Ala Pro Arg
 245 250 255
 10 Gln Glu Glu Phe His Gln Arg Ala Asn Val Thr Phe Thr Leu Ser Lys
 260 265 270
 Phe His Trp Cys Cys His His His Val Gln Val Gln Pro Phe Phe Ser
 275 280 285
 15 Ser Cys Leu Asn Asp Cys Leu Arg His Ala Val Thr Val Pro Cys Pro
 290 295 300
 20 Val Ile Ser Asn Thr Thr Val Pro Lys Pro Val Ala Asp Tyr Ile Pro
 305 310 315 320
 Leu Trp Val Tyr Gly Leu Ile Thr Leu Ile Ala Ile Leu Leu Val Gly
 325 330 335
 25 Ser Val Ile Val Leu Ile Ile Cys Met Thr Trp Arg Leu Ser Gly Ala
 340 345 350
 Asp Gln Glu Lys His Gly Asp Asp Ser Lys Ile Asn Gly Ile Leu Pro
 355 360 365
 30 Val Ala Asp Leu Thr Pro Pro Pro Leu Arg Pro Arg Lys Val Trp Ile
 370 375 380
 35 Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu Val Val Leu Lys Phe
 385 390 395 400
 Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu Val Ala Leu Asp Leu
 405 410 415
 40 Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val Met Thr Trp Val Ser
 420 425 430
 Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Ile Leu
 435 440 445
 45 Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala Ile Leu Gly Trp Ala
 450 455 460
 50 Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp Lys Pro Ala Gly Asp
 465 470 475 480
 Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro
 485 490 495
 55 Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser Gly Ile Cys Ser
 500 505 510
 60 Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr Ser Arg Tyr Pro Leu
 515 520 525

Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met
 530 535 540
 5 Phe Glu Pro Gly Arg Met His His Val Arg Glu Leu Thr Gly Asp Asn
 545 550 555 560
 Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys Glu Ala Val Leu Arg
 565 570 575
 10 Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp Phe Glu Arg Glu Asn
 580 585 590
 Leu Cys Leu Ala Asp Gly Gln Asp Leu Pro Ser Leu Asp Glu Glu Val
 595 600 605
 15 Phe Glu Asp Pro Leu Leu Pro Pro Gly Gly Gly Ile Val Lys Gln Gln
 610 615 620
 20 Pro Leu Val Arg Glu Leu Pro Ser Asp Gly Cys Leu Val Val Asp Val
 625 630 635 640
 Cys Val Ser Glu Glu Glu Ser Arg Met Ala Lys Leu Asp Pro Gln Leu
 645 650 655
 25 Trp Pro Gln Arg Glu Leu Val Ala His Thr Leu Gln Ser Met Val Leu
 660 665 670
 Pro Ala Glu Gln Val Pro Ala Ala His Val Val Glu Pro Leu His Leu
 675 680 685
 30 Pro Asp Gly Ser Gly Ala Ala Ala Gln Leu Pro Met Thr Glu Asp Ser
 690 695 700
 35 Glu Ala Cys Pro Leu Leu Gly Val Gln Arg Asn Ser Ile Leu Cys Leu
 705 710 715 720
 Pro Val Asp Ser Asp Asp Leu Pro Leu Cys Ser Thr Pro Met Met Ser
 725 730 735
 40 Pro Asp His Leu Gln Gly Asp Ala Arg Glu Gln Leu Glu Ser Leu Met
 740 745 750
 Leu Ser Val Leu Gln Gln Ser Leu Ser Gly Gln Pro Leu Glu Ser Trp
 755 760 765
 45 Pro Arg Pro Glu Val Val Leu Glu Gly Cys Thr Pro Ser Glu Glu Glu
 770 775 780
 50 Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser Ser
 785 790 795 800
 Pro Gln Pro Pro Glu Trp Leu Thr Glu Glu Glu Leu Glu Leu Gly
 805 810 815
 55 Glu Pro Val Glu Ser Leu Ser Pro Glu Glu Leu Arg Ser Leu Arg Lys
 820 825 830
 Leu Gln Arg Gln Leu Phe Phe Trp Glu Leu Glu Lys Asn Pro Gly Trp
 835 840 845
 60

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Asn Ser Leu Glu Pro Arg Arg Pro Thr Pro Glu Glu Gln Asn Pro Ser
 850 855 860

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 3223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
 (B) CLONE: IL-17R

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 93..2690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGGAGACCGG AATTCGGGA AAAGAAAGCC TCAGAACGTT CGCTCGCTGC GTCCCCAGCC 60

GGGGCCGAGC CCTCCGCGAC GCCACCCGGG CC ATG GGG GCC GCA CGC AGC CCG 113
 Met Gly Ala Ala Arg Ser Pro
 1 5

35

CCG TCC GCT GTC CCG GGG CCC CTG CTG GGG CTG CTC CTG CTG CTC CTG 161
 Pro Ser Ala Val Pro Gly Pro Leu Leu Gly Leu Leu Leu Leu Leu
 10 15 20

40

GGC GTG CTG GCC CCG GGT GGC GCC TCC CTG CGA CTC CTG GAC CAC CGG 209
 Gly Val Leu Ala Pro Gly Gly Ala Ser Leu Arg Leu Leu Asp His Arg
 25 30 35

45

GCG CTG GTC TGC TCC CAG CCG GGG CTA AAC TGC ACG GTC AAG AAT AGT 257
 Ala Leu Val Cys Ser Gln Pro Gly Leu Asn Cys Thr Val Lys Asn Ser
 40 45 50 55

50

ACC TGC CTG GAT GAC AGC TGG ATT CAC CCT CGA AAC CTG ACC CCC TCC 305
 Thr Cys Leu Asp Asp Ser Trp Ile His Pro Arg Asn Leu Thr Pro Ser
 60 65 70

55

TCC CCA AAG GAC CTG CAG ATC CAG CTG CAC TTT GCC CAC ACC CAA CAA 353
 Ser Pro Lys Asp Leu Gln Ile Gln Leu His Phe Ala His Thr Gln Gln
 75 80 85

GGA GAC CTG TTC CCC GTG GCT CAC ATC GAA TGG ACA CTG CAG ACA GAC 401
 Gly Asp Leu Phe Pro Val Ala His Ile Glu Trp Thr Leu Gln Thr Asp
 90 95 100

60

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	GCC AGC ATC CTG TAC CTC GAG GGT GCA GAG TTA TCT GTC CTG CAG CTG	449
	Ala Ser Ile Leu Tyr Leu Glu Gly Ala Glu Leu Ser Val Leu Gln Leu	
	105 110 115	
5	AAC ACC AAT GAA CGT TTG TGC GTC AGG TTT GAG TTT CTG TCC AAA CTG	497
	Asn Thr Asn Glu Arg Leu Cys Val Arg Phe Glu Phe Leu Ser Lys Leu	
	120 125 130 135	
10	AGG CAT CAC CAC AGG CGG TGG CGT TTT ACC TTC AGC CAC TTT GTG GTT	545
	Arg His His His Arg Arg Trp Arg Phe Thr Phe Ser His Phe Val Val	
	140 145 150	
15	GAC CCT GAC CAG GAA TAT GAG GTG ACC GTT CAC CAC CTG CCC AAG CCC	593
	Asp Pro Asp Gln Glu Tyr Glu Val Thr Val His His Leu Pro Lys Pro	
	155 160 165	
	ATC CCT GAT GGG GAC CCA AAC CAC CAG TCC AAG AAT TTC CTT GTG CCT	641
	Ile Pro Asp Gly Asp Pro Asn His Gln Ser Lys Asn Phe Leu Val Pro	
	170 175 180	
20	GAC TGT GAG CAC GCC AGG ATG AAG GTA ACC ACG CCA TGC ATG AGC TCA	689
	Asp Cys Glu His Ala Arg Met Lys Val Thr Thr Pro Cys Met Ser Ser	
	185 190 195	
25	GGC AGC CTG TGG GAC CCC AAC ATC ACC GTG GAG ACC CTG GAG GCC CAC	737
	Gly Ser Leu Trp Asp Pro Asn Ile Thr Val Glu Thr Leu Glu Ala His	
	200 205 210 215	
30	CAG CTG CGT GTG AGC TTC ACC CTG TGG AAC GAA TCT ACC CAT TAC CAG	785
	Gln Leu Arg Val Ser Phe Thr Leu Trp Asn Glu Ser Thr His Tyr Gln	
	220 225 230	
35	ATC CTG CTG ACC AGT TTT CCG CAC ATG GAG AAC CAC AGT TGC TTT GAG	833
	Ile Leu Leu Thr Ser Phe Pro His Met Glu Asn His Ser Cys Phe Glu	
	235 240 245	
	CAC ATG CAC CAC ATA CCT GCG CCC AGA CCA GAA GAG TTC CAC CAG CGA	881
	His Met His His Ile Pro Ala Pro Arg Pro Glu Glu Phe His Gln Arg	
	250 255 260	
40	TCC AAC GTC ACA CTC ACT CTA CGC AAC CTT AAA GGG TGC TGT CGC CAC	929
	Ser Asn Val Thr Leu Thr Leu Arg Asn Leu Lys Gly Cys Cys Arg His	
	265 270 275	
45	CAA GTG CAG ATC CAG CCC TTC TTC AGC AGC TGC CTC AAT GAC TGC CTC	977
	Gln Val Gln Ile Gln Pro Phe Phe Ser Ser Cys Leu Asn Asp Cys Leu	
	280 285 290 295	
50	AGA CAC TCC GCG ACT GTT TCC TGC CCA GAA ATG CCA GAC ACT CCA GAA	1025
	Arg His Ser Ala Thr Val Ser Cys Pro Glu Met Pro Asp Thr Pro Glu	
	300 305 310	
55	CCA ATT CCG GAC TAC ATG CCC CTG TGG GTG TAC TGG TTC ATC ACG GGC	1073
	Pro Ile Pro Asp Tyr Met Pro Leu Trp Val Tyr Trp Phe Ile Thr Gly	
	315 320 325	
	ATC TCC ATC CTG CTG GTG GGC TCC GTC ATC CTG CTC ATC GTC TGC ATG	1121
	Ile Ser Ile Leu Leu Val Gly Ser Val Ile Leu Leu Ile Val Cys Met	
	330 335 340	
60		

	ACC TGG AGG CTA GCT GGG CCT GGA AGT GAA AAA TAC AGT GAT GAC ACC	1169
	Thr Trp Arg Leu Ala Gly Pro Gly Ser Glu Lys Tyr Ser Asp Asp Thr	
	345 350 355	
5	AAA TAC ACC GAT GGC CTG CCT GCG GCT GAC CTG ATC CCC CCA CCG CTG	1217
	Lys Tyr Thr Asp Gly Leu Pro Ala Ala Asp Leu Ile Pro Pro Pro Leu	
	360 365 370	
10	AAG CCC AGG AAG GTC TGG ATC ATC TAC TCA GCC GAC CAC CCC CTC TAC	1265
	Lys Pro Arg Lys Val Trp Ile Ile Tyr Ser Ala Asp His Pro Leu Tyr	
	380 385 390	
15	GTG GAC GTG GTC CTG AAA TTC GCC CAG TTC CTG CTC ACC GCC TGC GGC	1313
	Val Asp Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly	
	395 400 405	
	ACG GAA GTG GCC CTG GAC CTG CTG GAA GAG CAG GCC ATC TCG GAG GCA	1361
	Thr Glu Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala	
	410 415 420	
20	GGA GTC ATG ACC TGG GTG GGC CGT CAG AAG CAG GAG ATG GTG GAG AGC	1409
	Gly Val Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser	
	425 430 435	
25	AAC TCT AAG ATC ATC GTC CTG TGC TCC CGC GGC ACG CGC GCC AAG TGG	1457
	Asn Ser Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp	
	440 445 450 455	
30	CAG GCG CTC CTG GGC CGG GGG GCG CCT GTG CGG CTG CGC TGC GAC CAC	1505
	Gln Ala Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His	
	460 465 470	
35	GGA AAG CCC GTG GGG GAC CTG TTC ACT GCA GCC ATG AAC ATG ATC CTC	1553
	Gly Lys Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu	
	475 480 485	
	CCG GAC TTC AAG AGG CCA GCC TGC TTC GGC ACC TAC GTA GTC TGC TAC	1601
	Pro Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr	
	490 495 500	
40	TTC AGC GAG GTC AGC TGT GAC GGC GAC GTC CCC GAC CTG TTC GGC GCG	1649
	Phe Ser Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala	
	505 510 515	
45	GCG CCG CGG TAC CCG CTC ATG GAC AGG TTC GAG GAG GTG TAC TTC CGC	1697
	Ala Pro Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg	
	520 525 530 535	
50	ATC CAG GAC CTG GAG ATG TTC CAG CCG GGC CGC ATG CAC CGC GTA GGG	1745
	Ile Gln Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly	
	540 545 550	
55	GAG CTG TCG GGG GAC AAC TAC CTG CGG AGC CCG GGC GGC AGG CAG CTC	1793
	Glu Leu Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu	
	555 560 565	
60	CGC GCC GCC CTG GAC AGG TTC CGG GAC TGG CAG GTC CGC TGT CCC GAC	1841
	Arg Ala Ala Leu Asp Arg Phe Arg Asp Trp Gln Val Arg Cys Pro Asp	
	570 575 580	

	TGG	TTC	GAA	TGT	GAG	AAC	CTC	TAC	TCA	GCA	GAT	GAC	CAG	GAT	GCC	CCG	1889
	Trp	Phe	Glu	Cys	Glu	Asn	Leu	Tyr	Ser	Ala	Asp	Asp	Gln	Asp	Ala	Pro	
	585						590					595					
5	TCC	CTG	GAC	GAA	GAG	GTG	TTT	GAG	GAG	CCA	CTG	CTG	CCT	CCG	GGA	ACC	1937
	Ser	Leu	Asp	Glu	Glu	Val	Phe	Glu	Glu	Pro	Leu	Leu	Pro	Pro	Gly	Thr	
	600					605					610					615	
10	GGC	ATC	GTG	AAG	CGG	GCG	CCC	CTG	GTG	CGC	GAG	CCT	GGC	TCC	CAG	GCC	1985
	Gly	Ile	Val	Lys	Arg	Ala	Pro	Leu	Val	Arg	Glu	Pro	Gly	Ser	Gln	Ala	
					620					625					630		
15	TGC	CTG	GCC	ATA	GAC	CCG	CTG	GTC	GGG	GAG	GAA	GGA	GGA	GCA	GCA	GTG	2033
	Cys	Leu	Ala	Ile	Asp	Pro	Leu	Val	Gly	Glu	Glu	Gly	Gly	Ala	Ala	Val	
				635					640					645			
	GCA	AAG	CTG	GAA	CCT	CAC	CTG	CAG	CCC	CGG	GGT	CAG	CCA	GCG	CCG	CAG	2081
	Ala	Lys	Leu	Glu	Pro	His	Leu	Gln	Pro	Arg	Gly	Gln	Pro	Ala	Pro	Gln	
			650					655					660				
20	CCC	CTC	CAC	ACC	CTG	GTG	CTC	GCC	GCA	GAG	GAG	GGG	GCC	CTG	GTG	GCC	2129
	Pro	Leu	His	Thr	Leu	Val	Leu	Ala	Ala	Glu	Glu	Gly	Ala	Leu	Val	Ala	
		665					670					675					
25	GCG	GTG	GAG	CCT	GGG	CCC	CTG	GCT	GAC	GGT	GCC	GCA	GTC	CGG	CTG	GCA	2177
	Ala	Val	Glu	Pro	Gly	Pro	Leu	Ala	Asp	Gly	Ala	Ala	Val	Arg	Leu	Ala	
	680					685				690						695	
30	CTG	GCG	GGG	GAG	GGC	GAG	GCC	TGC	CCG	CTG	CTG	GGC	AGC	CCG	GGC	GCT	2225
	Leu	Ala	Gly	Glu	Gly	Glu	Ala	Cys	Pro	Leu	Leu	Gly	Ser	Pro	Gly	Ala	
				700						705					710		
35	GGG	CGA	AAT	AGC	GTC	CTC	TTC	CTC	CCC	GTG	GAC	CCC	GAG	GAC	TCG	CCC	2273
	Gly	Arg	Asn	Ser	Val	Leu	Phe	Leu	Pro	Val	Asp	Pro	Glu	Asp	Ser	Pro	
				715					720					725			
	CTT	GGC	AGC	AGC	ACC	CCC	ATG	GCG	TCT	CCT	GAC	CTC	CTT	CCA	GAG	GAC	2321
	Leu	Gly	Ser	Ser	Thr	Pro	Met	Ala	Ser	Pro	Asp	Leu	Leu	Pro	Glu	Asp	
			730					735					740				
40	GTG	AGG	GAG	CAC	CTC	GAA	GGC	TTG	ATG	CTC	TCG	CTC	TTC	GAG	CAG	AGT	2369
	Val	Arg	Glu	His	Leu	Glu	Gly	Leu	Met	Leu	Ser	Leu	Phe	Glu	Gln	Ser	
		745					750					755					
45	CTG	AGC	TGC	CAG	GCC	CAG	GGG	GGC	TGC	AGT	AGA	CCC	GCC	ATG	GTC	CTC	2417
	Leu	Ser	Cys	Gln	Ala	Gln	Gly	Gly	Cys	Ser	Arg	Pro	Ala	Met	Val	Leu	
	760					765				770						775	
50	ACA	GAC	CCA	CAC	ACG	CCC	TAC	GAG	GAG	GAG	CAG	CGG	CAG	TCA	GTG	CAG	2465
	Thr	Asp	Pro	His	Thr	Pro	Tyr	Glu	Glu	Glu	Gln	Arg	Gln	Ser	Val	Gln	
					780					785					790		
55	TCT	GAC	CAG	GGC	TAC	ATC	TCC	AGG	AGC	TCC	CCG	CAG	CCC	CCC	GAG	GGA	2513
	Ser	Asp	Gln	Gly	Tyr	Ile	Ser	Arg	Ser	Ser	Pro	Gln	Pro	Pro	Glu	Gly	
				795					800					805			
60	CTC	ACG	GAA	ATG	GAG	GAA	GAG	GAG	GAA	GAG	GAG	CAG	GAC	CCA	GGG	AAG	2561
	Leu	Thr	Glu	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Asp	Pro	Gly	Lys	
			810				815						820				

CCG GCC CTG CCA CTC TCT CCC GAG GAC CTG GAG AGC CTG AGG AGC CTC 2609
 Pro Ala Leu Pro Leu Ser Pro Glu Asp Leu Glu Ser Leu Arg Ser Leu
 825 830 835

5 CAG CGG CAG CTG CTT TTC CGC CAG CTG CAG AAG AAC TCG GGC TGG GAC 2657
 Gln Arg Gln Leu Leu Phe Arg Gln Leu Gln Lys Asn Ser Gly Trp Asp
 840 845 850 855

10 ACG ATG GGG TCA GAG TCA GAG GGG CCC AGT GCA TGA GGGCGGCTCC 2703
 Thr Met Gly Ser Glu Ser Glu Gly Pro Ser Ala
 860 865

CCAGGGACCG CCCAGATCCC AGCTTTGAGA GAGGAGTGTG TGTGCACGTA TTCATCTGTG 2763

15 TGTACATGTC TGCATGTGTA TATGTTCTGTG TGTGAAATGT AGGCTTTAAA ATGTAAATGT 2823

CTGGATTTTA ATCCCAGGCA TCCCTCCTAA CTTTTCTTTG TGCAGCGGTC TGGTTATCGT 2883

20 CTATCCCCAG GGGAATCCAC ACAGCCCGCT CCCAGGAGCT AATGGTAGAG CGTCCTTGAG 2943

GCTCCATTAT TCGTTCATTC AGCATTTATT GTGCACCTAC TATGTGGCGG GCATTTGGGA 3003

TACCAAGATA AATTGCATGC GGCATGGCCC CAGCCATGAA GGAACCTAAC CGCTAGTGCC 3063

25 GAGGACACGT TAAACGAACA GGATGGGCCG GGCACGGTGG CTCACGCCTG TAATCCCAGC 3123

ACACTGGGAG GCCGAGGCAG GTGGATCACT CTGAGGTCAG GAGTTTGAGC CAGCCTGGCC 3183

AACATGGTGA AACCCCGGAA TTCGAGCTCG GTACCCGGGG 3223

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 866 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Ala Arg Ser Pro Pro Ser Ala Val Pro Gly Pro Leu Leu
 1 5 10 15

45 Gly Leu Leu Leu Leu Leu Leu Gly Val Leu Ala Pro Gly Gly Ala Ser
 20 25 30

50 Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln Pro Gly Leu
 35 40 45

Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
 50 55 60

55 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
 65 70 75 80

His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
 85 90 95

60

Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
 100 105 110
 5 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
 115 120 125
 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Phe
 130 135 140
 10 Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Glu Tyr Glu Val Thr
 145 150 155 160
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln
 165 170 175
 15 Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val
 180 185 190
 20 Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
 195 200 205
 Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp
 210 215 220
 25 Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
 225 230 235 240
 Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro Arg
 245 250 255
 30 Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn
 260 265 270
 35 Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser
 275 280 285
 Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro
 290 295 300
 40 Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp
 305 310 315 320
 Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val
 325 330 335
 45 Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser
 340 345 350
 50 Glu Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala
 355 360 365
 Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr
 370 375 380
 55 Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln
 385 390 395 400
 Phe Leu Leu Thr Ala Cys Gly Thr Glu Val Ala Leu Asp Leu Leu Glu
 405 410 415
 60

Glu Gln Ala Ile Ser Glu Ala Gly Val Met Thr Trp Val Gly Arg Gln
 420 425 430
 5 Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Val Leu Cys Ser
 435 440 445
 Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro
 450 455 460
 10 Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr
 465 470 475 480
 Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe
 485 490 495
 15 Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp
 500 505 510
 Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg
 515 520 525
 20 Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro
 530 535 540
 25 Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg
 545 550 555 560
 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp
 565 570 575
 30 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser
 580 585 590
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu
 595 600 605
 35 Pro Leu Leu Pro Pro Gly Thr Gly Ile Val Lys Arg Ala Pro Leu Val
 610 615 620
 40 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly
 625 630 635 640
 Glu Glu Gly Gly Ala Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro
 645 650 655
 45 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala
 660 665 670
 Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Leu Ala Asp
 675 680 685
 50 Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro
 690 695 700
 55 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro
 705 710 715 720
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser
 725 730 735
 60

Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met
740 745 750

5 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys
755 760 765

Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu
770 775 780

10 Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser
785 790 795 800

Ser Pro Gln Pro Pro Glu Gly Leu Thr Glu Met Glu Glu Glu Glu Glu
805 810 815

15 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp
820 825 830

20 Leu Glu Ser Leu Arg Ser Leu Gln Arg Gln Leu Leu Phe Arg Gln Leu
835 840 845

Gln Lys Asn Ser Gly Trp Asp Thr Met Gly Ser Glu Ser Glu Gly Pro
850 855 860

25 Ser Ala
865

30

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